

### **Amendments to the Claims**

*The following listing of claims replaces all prior versions and listings of the claims in this application.*

1. (Currently amended) A genetically modified plant cell having an increased activity of at least one Class 3 branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified, wherein the genetic modification is the introduction of at least one foreign nucleic acid molecule which codes a class 3 branching enzyme into the genome of the plant, and wherein the class 3 branching enzyme has an iso-amylase domain (Pfam acc.: Pf02922) and an alpha-amylase domain (Pfam acc: Pf00128) which are separated from one another by at least 100 amino acids.
2. (Canceled)
3. (Canceled)
4. (Currently amended) The genetically modified plant cell according to Claim 3 ~~1~~, wherein the said foreign nucleic acid molecule is
  - a) a nucleic acid molecule, which codes a protein with the amino acid sequence ~~given under of~~ Seq ID NO 4;
  - b) a nucleic acid molecule, which codes a protein, the amino acid sequence of which has an identity of at least ~~80%~~ 50% with the amino acid sequence ~~given under of~~ SEQ ID NO: 4;
  - c) a nucleic acid molecule, ~~which includes~~ comprising the nucleotide sequence of Seq ID NO: 3 or a complementary sequence thereof;
  - d) a nucleic acid molecule, the nucleic acid sequence of which has an identity of at least ~~80%~~ 50% with the nucleic acid sequences described under a) or c);
  - e) a nucleic acid molecule, which hybridizes with at least one strand of the nucleic acid molecules described under a) or c) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na<sub>2</sub>HPO<sub>4</sub>; 250 □ g/ml herring sperm DNA; 50 □ g/ml tRNA; or 25 M

sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS;

- f) a nucleic acid molecule, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; or
- g) a nucleic acid molecule, which represents fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

5. (Currently amended) The genetically modified plant cell according to Claim [[2]] 1, wherein said foreign nucleic acid molecule is a DNA molecule linked with regulatory sequences for transcription in vegetable cells

- ~~a) a T-DNA molecule, which leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome;~~
- ~~b) a DNA molecule, which contains transposons, which leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome;~~
- ~~c) a DNA molecule, which codes a Class 3 branching enzyme and which are linked with regulatory sequences, which guarantee transcription in vegetable cells and leads to an increase in Class 3 branching enzyme activity in the cell; or~~
- ~~d) a nucleic acid molecule introduced by means of in vivo mutagenesis, which leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.~~

6. (Previously presented) A plant cell according to Claim 1, which synthesizes a modified starch in comparison with corresponding wild type plant cells that have not been genetically modified.

7. (Previously presented) A plant containing plant cells according to Claim 1.

8. (Previously presented) A plant according to Claim 7, which is a starch-storing plant.

9. (Previously presented) A plant according to Claim 7, which is a maize, rice, wheat, rye, oat, barley, cassava, potato, sago, mung bean, pea or sorghum plant.

10. (Previously presented) The plant according to Claim 9, which is a potato plant.
11. (Previously presented) Propagation material of plants according to Claim 7.
12. (Previously presented) Harvestable plant parts of plants according to Claim 7.
13. (Currently amended) A method for the manufacture of a genetically modified plant ~~according to Claim 5 to 8~~, comprising
  - a) genetically modifying a plant cell, by introducing at least one foreign nucleic acid molecule which codes a class 3 branching enzyme into the genome of the plant cell, wherein the class 3 branching enzyme has an iso-amylase domain (Pfam acc.: Pf02922) and an alpha-amylase domain (Pfam acc: Pf00128) which are separated from one another by at least 100 amino acids, whereby the genetic modification leads to an increase in the activity of a Class 3 vegetable branching enzyme in comparison with corresponding wild type plant cells that have not been genetically modified;
  - b) regenerating a plant from plant cells from Step a); and
  - c) if necessary, producing further plants with ~~the help of~~ the plants according to Step b).
14. (Canceled)
15. (Currently amended) The method according to Claim ~~14~~ 13, wherein the said foreign nucleic acid molecule is
  - a) a nucleic acid molecule, which codes a protein with the amino acid sequence of Seq ID NO 4;
  - b) a nucleic acid molecule, which codes a protein, the amino acid sequence of which has an identity of at least ~~80%~~ 50% with the amino acid sequence of SEQ ID NO: 4;
  - c) a nucleic acid molecule, ~~which includes~~ comprising the nucleotide sequence ~~shown under~~ of Seq ID NO 3 or a complementary sequence thereof;
  - d) a nucleic acid molecule, the nucleic acid sequence of which has an identity of at least 80% ~~50%~~ with the nucleic acid sequences described under a) or c);
  - e) a nucleic acid molecule, which hybridizes with at least one strand of the nucleic acid

molecules described under a) or c) under stringent conditions, wherein said stringent conditions are conducting the hybridization reaction at 65°C-68°C in a solution comprising 2X SSC 10X Denhardt solution (Ficoll 400+PEG+BSA; Ratio 1:1:1); 0.1% SDS; 5 mM EDTA; 50 mM Na<sub>2</sub>HPO<sub>4</sub>; 250 µg/ml herring sperm DNA; 50 µg/ml tRNA; or 25 M sodium phosphate buffer pH 7.2; 1 mM EDTA; 7% SDS, and washing at 65°C-68°C in a solution comprising 0.2X SSC and 0.1% SDS;

- f) a nucleic acid molecule, the nucleotide sequence of which deviates from the sequence of the nucleic acid molecules identified under a), b), c), d), e) or f) due to the degeneration of the genetic code; or
- g) a nucleic acid molecule, which represents fragments, allelic variants and/or derivatives of the nucleic acid molecules identified under a), b), c), d), e) or f).

16. (Currently amended) The method according to Claim 44 13, wherein said foreign nucleic acid molecule is a DNA molecule linked with regulatory sequences for transcription in vegetable cells

- ~~a) a T-DNA molecule, which leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome;~~
- ~~b) a DNA molecule, which contains transposons, which leads to an increase in the expression of a Class 3 branching enzyme gene due to integration in the vegetable genome;~~
- ~~c) a DNA molecule, which codes a Class 3 branching enzyme and which are linked with regulatory sequences, for transcription in vegetable cells and leads to an increase in Class 3 branching enzyme activity in the cell; or~~
- ~~d) a Nucleic acid molecule introduced by means of in vivo mutagenesis, which leads to a mutation or an insertion of a heterologous sequence in at least one endogenous gene coding a Class 3 branching enzyme, wherein the mutation or insertion effects an increase in the expression of a gene coding a Class 3 branching enzyme.~~

17. (Previously presented) A method according to Claim 13, wherein the genetically modified plant synthesizes a modified starch in comparison with corresponding wild type plants that have not been genetically modified.

18. (Previously presented) A modified starch obtainable from a genetically modified plant according to Claim 7, from propagation material according to Claim 11, or from harvestable plant parts according to Claim 12.
19. (Previously presented) A method for the manufacture of a modified starch including the step of extracting the starch from a plant cell according to Claim 1.
20. (Previously presented) A method for the manufacture of a modified starch including the step of extracting the starch from a plant according to Claim 7.
21. (Previously presented) A method for the manufacture of a modified starch including the step of extracting the starch from harvestable plant parts according to Claim 12.
22. (Previously presented) A method for the manufacture of a derived starch, wherein modified starch according to Claim 18 or obtainable by the method according to Claim 19 is derived.
23. (Canceled)
24. (Previously presented) A modified starch obtainable by the method according to Claim 19.
25. (Previously presented) Derived starch obtainable by the method according to Claim 22.
26. (Canceled)
27. (New) The method of claim 1, wherein the foreign nucleic acid molecule is
  - a) a nucleic acid molecule, which codes a protein, the amino acid sequence of which has an identity of at least 90% with the amino acid sequence of SEQ ID NO: 4; or
  - b) a nucleic acid molecule, which has an identity of at least 90% with the nucleic acid sequence of SEQ ID NO: 3 or a complement thereof.
28. (New) The method of claim 1, wherein the foreign nucleic acid molecule is
  - a) a nucleic acid molecule, which codes a protein, the amino acid sequence of which has an identity of at least 95% with the amino acid sequence of SEQ ID NO: 4; or
  - b) a nucleic acid molecule, which has an identity of at least 95% with the nucleic acid sequence of SEQ ID NO: 3 or a complement thereof.